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## RAW SEQUENCE LISTING

DATE: 08/20/2004

PATENT APPLICATION: US/10/777,195

TIME: 09:08:49

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08202004\J777195.raw

## SEQUENCE LISTING

## 12 (1) GENERAL INFORMATION:

14 (i) APPLICANT: Takashi OKADO et al.

16 (ii) TITLE OF INVENTION: GENE REGULATING AUREOBASIDIN SENSITIVITY  
17 (AS AMENDED)

20 (iii) NUMBER OF SEQUENCES: 50

22 (iv) CORRESPONDENCE ADDRESS:

24 (A) ADDRESSEE: WENDEROTH, LIND &amp; PONACK, L.L.P.

26 (B) STREET: 2033 K Street, N.W., #800

28 (C) CITY: Washington

30 (D) STATE: D.C.

32 (E) COUNTRY: U.S.A.

34 (F) ZIP: 20006

36 (v) COMPUTER READABLE FORM:

38 (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

40 (B) COMPUTER: IBM Compatible

42 (C) OPERATING SYSTEM: MS-DOS

44 (D) SOFTWARE: Wordperfect 5.1

46 (vi) CURRENT APPLICATION DATA:

C--&gt; 48 (A) APPLICATION NUMBER: US/10/777,195

C--&gt; 50 (B) FILING DATE: 13-Feb-2004

C--&gt; 58 (vii) PRIOR APPLICATION DATA:

54 (A) APPLICATION NUMBER: 09/368,431

56 (B) FILING DATE: August 5, 1999

60 (A) APPLICATION NUMBER: 08/716,873

62 (B) FILING DATE: \

C--&gt; 64 (viii) ATTORNEY/AGENT INFORMATION:

66 (A) NAME: Warren M. Cheek, Jr.

68 (B) REGISTRATION NUMBER: 33,367

70 (C) REFERENCE/DOCKET NUMBER: 2003-1772/WMC/00001

C--&gt; 72 (ix) TELECOMMUNICATION INFORMATION:

74 (A) TELEPHONE: 202-721-8200

76 (B) TELEFAX: 202-721-8250

78 (C) TELEX:

80 (2) INFORMATION FOR SEQ ID NO: 1:

82 (i) SEQUENCE CHARACTERISTICS:

84 (A) LENGTH: 4140 base pairs

86 (B) TYPE: nucleic acid

88 (C) STRANDEDNESS: double

90 (D) TOPOLOGY: linear

92 (ii) MOLECULE TYPE: Genomic DNA

C--&gt; 95 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

C--&gt; 98 AGATCTGTGG CTTCCGGTTG GCTACTTGTA ACCAACTGAT GGTCAGATGG ATCTGCCGTC 60

(ps.6)

**ENTERED**

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100	TGTTTTGATT	TGAATTTTCC	CTGCTCATT	TGATTCTGTG	AGAGGCTGCA	TTCATTATCA	120
102	CATCTCATAC	CCGGCGCCTG	CGACTTCGGT	CACCTCTGCG	GTCTGGCGGT	TACCGGGGTC	180
104	CGTCTGAGAC	TCGTCACTCA	GCCATTTCGAG	TATGCGAACT	CTGACTTTGC	TCACCTAAGA	240
106	GTTTGCACGA	GATGCCGAAA	TCCTCCTCGA	GTAGAGTTTG	CAAGGCTTGA	ACCTTGGTCC	300
108	TTGAAGCCCG	AAAGTGCTC	AGTAGTGGGA	TCGATAGTCT	GGTTGTTGAA	GATTTTCTCC	360
110	TCCACCTTAC	CTATGGCCGC	TGGCCTTCTC	CACCTTTCAG	GCTTTCAGGC	ACCCTCGGCT	420
112	CGGATTCTGT	ATCGTCCGGT	ACCGAAGCTA	GTCCTAGCTA	GTCAAAGCTA	GTCCAAGCTA	480
114	GTCTCGTCAA	GGTTTGCGC	AGCGCGGTTC	CGTGTAAGT	ACAAATTTGA	AATACGAATA	540
116	CGCAGTACTC	GCAGCCGGCA	CTTCCGCTCA	GCCCAGGCTC	AGAGGCTAAG	GGTGTTGGCG	600
118	CTTCCTCATC	ATCTTCTTCT	CGTCGACCTT	TTCTCTTTTC	TCTCCCTATC	GGTGCTTCTC	660
120	TCCAACCTCA	TTCTCAGTCG	TTCGCCCATC	AGGTTTATAC	TCCGGCTCCG	TGGCCATCTG	720
122	CCTCCCTCAC	GACCTCCTCG	TTCCAGGTTT	TCCTCTCGAC	TGCTGCGCCC	TTGCACTTCG	780
124	CCTTGTCATCA	GTGAAACCCC	CTGCAACGTG	ACGGCTCAAA	GACATCCTCG	TTTGGCCGCT	840
126	GGAGACCGGA	GCGTGCGCTT	CGTTTCGTCT	TCTTCGAACC	GATCTCAATT	TCCCCGCTCG	900
128	GGTTGACGCC	GTCAGCACCC	TGCTCGTTGC	CTAACGGCTT	GTTATTCAAG	ACCCCTTTTC	960
130	TGCCGCTTCC	GCGACCGATT	TATTCGTGCG	CTTCCAACCTC	TTGTACAATC	GGGGGGAAAG	1020
132	AAAGCAGACG	GAGTTCGATC	TGGAGGAATT	ATAGCTGAGT	CTTGCCCGCA	AGACTCGCCG	1080
134	CAACCATGAA	TCAAACACTT	CCCACGTGGA	AGGACCGCAC	GCAGAACCAG	TTTGGAAAGC	1140
136	TTCAGATCCA	GGTTCCATGG	CGTCCATCC	AACTGCTCGT	CCCGCATCGC	ATGCGGCGGA	1200
138	AGTTAAGGTC	CAAATTGCGC	AGTAGAGCGT	CTCCTACCTC	GTCAATAGCC	TCTTTACAGA	1260
140	CGTCGTTATC	GCCTGCAGAC	ACACTACGAT	CGCTCCAAAG	CCACCGATGG	ACGGTTTACG	1320
142	ACTTCCAATA	TCGTCTTCTG	TTGATCGTGG	GCATCTTCTC	TTTGACCGTT	ATCGAGTCGC	1380
144	CCGGGCCTTT	GGGCAAAACG	GCCATTTTCT	CCATGCTCCT	ATTCTCTCTC	CTGATCCCTA	1440
146	TGACCCGCCA	GTTCTTCTC	CCGTTTCTGC	CGATTGCCGG	ATGGCTTCTG	TTTTTCTACG	1500
148	CCTGCCAGTG	AGTTAAAAAC	AACCCGCTAC	CAGACCCCGT	GCAGCAGTTA	CTCACATATG	1560
150	CAGGTTTCAT	CCAAGCGATT	GGCGCCCTGC	GATTTGGGTT	CGTGTCTTGC	CTGCACTGGA	1620
152	GAATATTCTC	TACGGCGCAA	ACATCAGCAA	CATCCTATCC	GCTCACCAGA	ACGTTGTGCT	1680
154	TGACGTGCTG	GCGTGGCTAC	CCTACGGTAT	CTGCCACTAT	GGCGCTCCGT	TTGTGTGCTC	1740
156	GTTGATCATG	TTATCTTCTG	GTCCGCCCGG	CACTGTTCCC	CTTTTCGCGC	GCACTTTCGG	1800
158	CTATATCAGT	ATGACTGCGG	TTACTATTCA	GCTGTTTTTC	CCTTGCTCTC	CACCTTGGTA	1860
160	TGAGAATCGC	TATGGTCTAG	CTCCGGCAGA	CTACTCCATC	CAAGGTGATC	CCGCAGGGCT	1920
162	TGCCCGCATT	GACAAGCTTT	TCGGCATCGA	CCTTTACACG	TCTGTTTTCC	ATCAGTCGCC	1980
164	TGTTGTGTTT	GGCGCTTTTC	CGTCGCTGCA	TGCTGCCGAC	TCAACCCTGG	CCGCACTTTT	2040
166	CATGAGTCAT	GTTTTCCCCC	GCATGAAGCC	CGTCTTCGTG	ACCTATACTC	TATGGATGTG	2100
168	GTGGGCAACA	ATGTACCTCT	CACATCACTA	TGCGGTCGAT	TTGGTTGCGG	GTGGTCTCCT	2160
170	GGCCGCCATT	GCTTTCTACT	TCGCCAAGAC	CCGATTCCCT	CCCCGTGTCC	AGCTCGACAA	2220
172	GACCTTCCGT	TGGGACTACG	ACTATGTGGA	ATTCCGCGAG	TCTGCCCTGG	AGTATGGGTA	2280
174	TGGTGCAGCT	GGCTATGATG	GAGACTTCAA	TCTCGACAGC	GATGAATGGA	CTGTTGGTTC	2340
176	TTCATCCTCC	GTCTCCTCAG	GCTCCTTGAG	TCCCCTTGAC	GATCATTACT	CATGGGAAAC	2400
178	CGAGGCACTG	ACCTCCCCAC	ATACTGATAT	TGAGTCCGGC	AGGCATACTT	TCAGCCCTTG	2460
180	AGTAGCCACA	AACCAAACCT	GATACCTGCA	TATAGCGATC	TCGCTCCTCC	TCCACTGCAT	2520
182	CTATTTACGA	GACGGCGTTA	GAACATTTCA	CGACATTCTG	GCTTTATTGC	ATCGAGCACA	2580
184	TTTCGACACA	TATATCTTTA	ATACCCTTTC	TTCCGGTGCC	CAGATCATCG	GTTTCGACCTT	2640
186	AATGTACCTC	GGTCCGAATC	CGCCTGGGAT	ACTGTTTTCT	TTTCCGCCGC	ACTTCACTGT	2700
188	ACATTGCTTG	ACATTGCGAA	ACCGGGTTGG	GCTCGAACGT	GGGATGGGTT	ATCGCTCATC	2760
190	GCTACACGCC	GTTGCTCCAT	CATAATGTTA	ATGGACACAA	TGGGGCTACG	CATCCTGGTG	2820
192	TTTAGTCTCG	GAAGACCATC	CGATAACCCC	CGTCGGTAAC	ACTCGCTTGT	CTCGTGTTCA	2880
194	CCCAGACACT	ACTTCAATTC	TCACTTCTAT	CGTCCGCTAT	TACCTTGACC	TGGTCGAACC	2940
196	CATCCTTATT	ATTCGTTTCG	ACTATGCTAT	ATATTTATTT	TTACCATTTCG	TGTCGATCGC	3000

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```

198 TCATACTCTT GGCGCTTGGG ACTGGAAGCA TTTATATTGG AAAAAATCAC GGAATGGGGC 3060
200 GCCTTTTCTT CTTGCACTTC ACTCGCTGTG CATAGACGGT TTTACATTTC TGCTTTGCAA 3120
202 TGCATCACGA ACTCTGCATT AGCATATAGA AAGAGGGGAA GGATGGACCT TCTTCTTGAT 3180
204 TGCTCGCATG GTTTATCCAT TCGCTCAAAG TGGATTACGT CCACATATTA CCCGGGGGCT 3240
206 ATACACATGG CTACTGTGTT GCTTTCTGAC ATTCCGCCGA CGTGCAAGGT TGGGAGGAGA 3300
208 GTCTGACGCT GACGGGGCTT GTTGAAGGAT GTTCACGCGT CCCGATTGTA CCCGGCTTCG 3360
210 ACTAACCTCA GATTCTCGAC TTGTTGGACG GTGACTTGAC TTGCTTGCTA TGGTCTGACG 3420
212 CTCTCACACC TACCTATCAC ATCCTCCTCA CCTCACAAAT TCCGCTCATG GACACTATCC 3480
214 TCTTCTTTTC GTTTCCTTG GATAGTGTGT GTGTGTGTGT GGTGCGGCA AATTATCCAT 3540
216 AGCAGCAGTA TTATTAGTTA TAATCCGGTA GTGTTATGAT TTATGAAGGC AACTTGTATA 3600
218 CTATTGCCAC TTTGTCCATA TCTCTTGCTT GTAATAGAAC TGACATCGCG ACGCTTCGGC 3660
220 CACGATGCAT ATAAAACTC TAGTCAACAC GATATTAACA AGCGAAACCA TTACGCTGTA 3720
222 AACTATTGAG GATCGCCGCG GGCCCATCTG GGACTTGACT GTACTAAATA TGTCTAAAG 3780
224 CAAGCAGACT AAATATTTAA CGTGGGATAT TATTCATATA CGCATATGTA TACATAGTCA 3840
226 TAACAAGCCA AGGGGTGGGT AGGGGTGGGT AATTATTATT TTTTTCGTC GATACAAGTA 3900
228 TCCATCCTTA AATGTCCGTG GTCTACTCTT CATAAATCTT AACCCGCTCC GCATACTCCT 3960
230 TTATCCTCGA GACAAAAGTG TCTTCAATTT CATCGCCACG GCCACCAGCA ACGCGGAGGA 4020
232 TAAGGTCGTT GAGAGAGGCG CGGCCGAGAA TGTCGACATG GTCGCCTTCA TATTGTTAGC 4080
234 ATGCGACGTC AGACTGGAAC CAGGAAGGGA AAGGAGAGAG GTACCTGTAT TTGGACCACC 4140

```

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 439 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

256 Met Asn Gln Thr Leu Pro Thr Trp Lys Asp Arg Thr Gln Asn Gln
258 1 5 10 15
260 Phe Gly Lys Leu Gln Ile Gln Val Pro Trp Arg Ser Ile Gln Leu
262 20 25 30
264 Leu Val Pro His Arg Met Arg Arg Lys Leu Arg Ser Lys Leu Arg
266 35 40 45
268 Ser Arg Ala Ser Pro Thr Ser Ser Ile Ala Ser Leu Gln Thr Ser
270 50 55 60
272 Leu Ser Pro Ala Asp Thr Leu Arg Ser Leu Gln Ser His Arg Trp
274 65 70 75
276 Thr Val Tyr Asp Phe Gln Tyr Leu Leu Leu Ile Val Gly Ile
278 80 85 90
280 Phe Ser Leu Thr Val Ile Glu Ser Pro Gly Pro Leu Gly Lys Thr
282 95 100 105
284 Ala Ile Phe Ser Met Leu Leu Phe Ser Leu Leu Ile Pro Met Thr
286 110 115 120
288 Arg Gln Phe Phe Leu Pro Phe Leu Pro Ile Ala Gly Trp Leu Leu
290 125 130 135
292 Phe Phe Tyr Ala Cys Gln Phe Ile Pro Ser Asp Trp Arg Pro Ala
294 140 145 150
296 Ile Trp Val Arg Val Leu Pro Ala Leu Glu Asn Ile Leu Tyr Gly
298 155 160 165

```

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```

300      Ala Asn Ile Ser Asn Ile Leu Ser Ala His Gln Asn Val Val Leu
302                      170                      175                      180
304      Asp Val Leu Ala Trp Leu Pro Tyr Gly Ile Cys His Tyr Gly Ala
306                      185                      190                      195
308      Pro Phe Val Cys Ser Leu Ile Met Phe Ile Phe Gly Pro Pro Gly
310                      200                      205                      210
312      Thr Val Pro Leu Phe Ala Arg Thr Phe Gly Tyr Ile Ser Met Thr
314                      215                      220                      225
316      Ala Val Thr Ile Gln Leu Phe Phe Pro Cys Ser Pro Pro Trp Tyr
318                      230                      235                      240
320      Glu Asn Arg Tyr Gly Leu Ala Pro Ala Asp Tyr Ser Ile Gln Gly
322                      245                      250                      255
324      Asp Pro Ala Gly Leu Ala Arg Ile Asp Lys Leu Phe Gly Ile Asp
326                      260                      265                      270
328      Leu Tyr Thr Ser Val Phe His Gln Ser Pro Val Val Phe Gly Ala
330                      275                      280                      285
332      Phe Pro Ser Leu His Ala Ala Asp Ser Thr Leu Ala Ala Leu Phe
334                      290                      295                      300
336      Met Ser His Val Phe Pro Arg Met Lys Pro Val Phe Val Thr Tyr
338                      305                      310                      315
340      Thr Leu Trp Met Trp Trp Ala Thr Met Tyr Leu Ser His His Tyr
342                      320                      325                      330
344      Ala Val Asp Leu Val Ala Gly Gly Leu Leu Ala Ala Ile Ala Phe
346                      335                      340                      345
348      Tyr Phe Ala Lys Thr Arg Phe Leu Pro Arg Val Gln Leu Asp Lys
350                      350                      355                      360
352      Thr Phe Arg Trp Asp Tyr Asp Tyr Val Glu Phe Gly Glu Ser Ala
354                      365                      370                      375
356      Leu Glu Tyr Gly Tyr Gly Ala Ala Gly Tyr Asp Gly Asp Phe Asn
358                      380                      385                      390
360      Leu Asp Ser Asp Glu Trp Thr Val Gly Ser Ser Ser Ser Val Ser
362                      395                      400                      405
364      Ser Gly Ser Leu Ser Pro Val Asp Asp His Tyr Ser Trp Glu Thr
366                      410                      415                      420
368      Glu Ala Leu Thr Ser Pro His Thr Asp Ile Glu Ser Gly Arg His
370                      425                      430                      435
372      Thr Phe Ser Pro

```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2856 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

C--> 396  GGTTTATACT CCGGCTCCGT GGCCATCTGC CTCCCTCACG ACCTCCTCGT TCCAGGTTTT    60
398  CCTCTCGACT GCTGCGCCCT TGCACTTCGC CTTCGATCAG TGAAACCCCC TGCAACGTGA    120
400  CGGCTCAAAG ACATCCTCGT TTGGCCGCTG GAGACCGGAG CGTGCGCTTC GTTTCGTCTT    180
402  CTTCGAACCG ATCTCAATTT CCCCCTCGG GTTGACGCCG TCAGCACCTT GCTCGTTGCC    240

```

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08202004\J777195.raw

```

404 TAACGGCTTG TTATTCAAGA CCCCTTTTCT GCCGCTTCCG CGACCGATTT ATTCGTCGCC 300
406 TTCCAACCTCT TGTACAATCG GGGGGAAAGA AAGCAGACGG AGTTCGATCT GGAGGAATTA 360
408 TAGCTGAGTC TTGCCCCGAA GACTCGCCGC AACCATGAAT CAAACACTTC CCACGTGGAA 420
410 GGACCGCAGC CAGAACCAGT TTGGAAAGCT TCAGATCCAG GTTCCATGGC GGTCCATCCA 480
412 ACTGCTCGTC CCGCATCGCA TCGGGCGGAA GTTAAGGTCC AAATTGCGCA GTAGAGCGTC 540
414 TCCTACCTCG TCAATAGCCT CTTTACAGAC GTCGTTATCG CCTGCAGACA CACTACGATC 600
416 GCTCCAAAGC CACCGATGGA CGGTTTACGA CTTCCAATAT CTGCTTCTGT TGATCGTGGG 660
418 CATCTTCTCT TTGACCGTTA TCGAGTCGCC CGGGCCTTTG GGCAAAACGG CCATTTTCTC 720
420 CATGCTCCTA TTCTCTCTCC TGATCCCTAT GACCCGCCAG TTCTTCTTCC CGTTTCTGCC 780
422 GATTGCCGGA TGGCTTCTGT TTTTCTACGC CTGCCAGTTC ATCCCAAGCG ATTGGCGCCC 840
424 TGCGATTTGG GTTCGTGTCT TGCCTGCACT GGAGAATATT CTCTACGGCG CAAACATCAG 900
426 CAACATCCTA TCCGCTCACC AGAACGTTGT GCTTGACGTG CTGGCGTGGC TACCCTACGG 960
428 TATCTGCCAC TATGGCGCTC CGTTTGTGTG CTCGTTGATC ATGTTCACTC TCGGTCCGCC 1020
430 CGGCACTGTT CCCCTTTTCG CGCGCACTTT CGGCTATATC AGTATGACTG CGGTTACTAT 1080
432 TCAGCTGTTT TTCCCTTGCT CTCCACCTTG GTATGAGAAT CGCTATGGTC TAGCTCCGGC 1140
434 AGACTACTCC ATCCAAGGTG ATCCCGCAGG GCTTGCCCGC ATTGACAAGC TTTTCGGCAT 1200
436 CGACCTTTAC ACGTCTGTTT TCCATCAGTC GCCTGTTGTG TTCGGCGCTT TTCCGTCGCT 1260
438 GCATGCTGCC GACTCAACCC TGGCCGCACT TTTTCATGAGT CATGTTTTCC CCCGCATGAA 1320
440 GCCCGTCTTC GTGACCTATA CTCTATGGAT GTGGTGCGCA ACAATGTACC TCTCACATCA 1380
442 CTATGCGGTC GATTTGGTG CCGGTGGTCT CCTGGCCGCC ATTGCTTTCT ACTTCGCCAA 1440
444 GACCCGATTC CTCCCCGTG TCCAGCTCGA CAAGACCTTC CGTTGGGACT ACGACTATGT 1500
446 GGAATTCGGC GAGTCTGCCC TGGAGTATGG GTATGGTGCA GCTGGCTATG ATGGAGACTT 1560
448 CAATCTCGAC AGCGATGAAT GGACTGTTGG TTCTTCATCC TCCGTCTCCT CAGGCTCCTT 1620
450 GAGTCCCGTT GACGATCAT ACTCATGGGA AACCGAGGCA CTGACCTCCC CACATACTGA 1680
452 TATTGAGTCC GGCAGGCATA CTTTCAGCCC TTGAGTAGCC ACAAACCAA CTCGATACCT 1740
454 GCATATAGCG ATCTCGTCC TCCTCCACTG CATCTATTTA CGAGACGGCG TTAGAACATT 1800
456 TCACGACATT CTGGCTTTAT TGCATCGAGC ACATTTTCGAC ACATATATCT TTAATACCCT 1860
458 TTCTTCGGTG TCCCAGATCA TCGGTTTCGAC CTTAATGTAC CTCGGTCCGA ATCCGCCTGG 1920
460 GATACTGTTT CTCTTTCCGC CGCACTTCAC TGTACATTGC TTGACATTGC GAAACCGGGT 1980
462 TGGGCTCGAA CGTGGGATGG GTTATCGCTC ATCGCTACAC GCCGTTGCTC CATCATAATG 2040
464 TTAATGGACA CAATGGGGCT ACGCATCCTG GTGTTTAGTC CTGGAAGACC ATCCGATAAC 2100
466 CCCCGTCGGT AACACTCGCT TGTCTCGTGT CCACCCAGAC ACTACTTCAA TTCTCACTTC 2160
468 TATCGTCCGC TATTACCTTG ACCTGGTCTG ACCCATCCTT ATTATTTCGTT TCGACTATGC 2220
470 TATATATTTA TTTTTACCAT TCGTGTCGAT CGCTCATACT CTTGGCGCTT GGGACTGGAA 2280
472 GCATTTATAT TGGAAAAAAT CACGGAATGG GGCGCCTTTT CTTCTTGCAC TTCACTCGCT 2340
474 GTGCATAGAC GGTTTTACAT TTCTGCTTTG CAATGCATCA CGAACTCTGC ATTAGCATAT 2400
476 AGAAAGAGGG GAAGGATGGA CCTTCTTCTT GATTGCTCGC ATGGTTTATC CATTGCTCA 2460
478 AAGTGGATTA CGTCCACATA TTACCCGGGG GCTATACACA TGGCTACTGT GTTGCTTTCT 2520
480 GACATTCGCC GGACGTGCAA GGTGGGAGG AGAGTCTGAC GCTGACGGGG CTTGTTGAAG 2580
482 GATGTTACG CGTCCCGATT TGACCCGGCT TCGACTAACC TCAGATTCTC GACTTGTTGG 2640
484 ACGGTGACTT GACTTGCTTG CTATGGTCTG ACGCTCTCAG ACCTACCTAT CACATCCTCC 2700
486 TCACCTCACA AATTCCGCTC ATGGACACTA TCCTCTTCTT TTCGTTTCCC TTGGATAGTG 2760
488 TGTGTGTGTG TGTGGTTGGG GCAAATTATC CATAGCAGCA GTATTATTAG TTATAATCCG 2820
490 GTAGTGTTAT GATTTATGAA GGCAACTTGT ATACTA 2856

```

494 (2) INFORMATION FOR SEQ ID NO: 4:

496 (i) SEQUENCE CHARACTERISTICS:

498 (A) LENGTH: 439 amino acids

500 (B) TYPE: amino acid

502 (C) STRANDEDNESS: single

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/777,195

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Input Set : A:\PTO.AMC.txt  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos.3,7  
Seq#:11; Xaa Pos.5,9  
Seq#:25; N Pos. 18,24  
Seq#:26; N Pos. 18,21

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/777,195

DATE: 08/20/2004

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08202004\J777195.raw

L:48 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:50 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:52 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:58 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]  
L:64 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]  
L:72 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]  
L:95 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
L:98 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=1  
L:396 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=3  
L:1220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0  
L:1288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
L:1312 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=12  
L:1432 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=13  
L:1550 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=14  
L:1666 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=15  
L:1900 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=17  
L:2134 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=19  
L:2360 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=21  
L:2586 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=23  
L:3200 M:111 C: (47) String data converted to upper case,  
L:3222 M:111 C: (47) String data converted to upper case,  
L:3244 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=27  
L:3488 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=29  
L:3564 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=31  
L:3640 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=32  
L:3764 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=35  
L:3984 M:111 C: (47) String data converted to upper case,  
L:4006 M:111 C: (47) String data converted to upper case,  
L:4028 M:111 C: (47) String data converted to upper case,  
L:4050 M:111 C: (47) String data converted to upper case,  
L:4072 M:111 C: (47) String data converted to upper case,  
L:4350 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=44

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Input Set : A:\PTO.AMC.txt

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L:4412 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=45  
L:4474 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=46  
L:4536 M:111 C: (47) String data converted to upper case,  
M:111 Repeated in SeqNo=47  
L:4598 M:111 C: (47) String data converted to upper case,  
L:4620 M:111 C: (47) String data converted to upper case,  
L:4642 M:111 C: (47) String data converted to upper case,